



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Boo

Search

Protein

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

default

Save

Text

Add to Clipboard

Get Subsequence

☐ 1: P46955. NCA3 protein, mit...[gi:1171667]

Links

LOCUS NCA3_YEAST 337 aa linear PLN 15-JUN-2002
 DEFINITION NCA3 protein, mitochondrial precursor.
 ACCESSION P46955
 VERSION P46955 GI:1171667
 DBSOURCE swissprot: locus NCA3_YEAST, accession P46955;
 class: standard.
 created: Nov 1, 1995.
 sequence updated: Nov 1, 1995.
 annotation updated: Jun 15, 2002.
 xrefs: gi: [439110](#), gi: [1094213](#), gi: [1008305](#), gi: [1008306](#), gi:
[968904](#), gi: [968906](#)
 xrefs (non-sequence databases): SGD S0003652
 KEYWORDS Mitochondrion; Transit peptide.
 SOURCE Saccharomyces cerevisiae.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (residues 1 to 337)
 AUTHORS Pelissier,P., Camougrand,N., Velours,G. and Guerin,M.
 TITLE NCA3, a nuclear gene involved in the mitochondrial expression of
 subunits 6 and 8 of the Fo-F1 ATP synthase of S. cerevisiae
 JOURNAL Curr. Genet. 27 (5), 409-416 (1995)
 MEDLINE [96059344](#)
 PUBMED [7586026](#)
 REMARK SEQUENCE FROM N.A.
 REFERENCE 2 (residues 1 to 337)
 AUTHORS Cziepluch,C., Kordes,E., Pujol,A. and Jauniaux,J.C.
 TITLE Sequencing analysis of a 40.2 kb fragment of yeast chromosome X
 reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2,
 SPT10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes,
 three remnant delta elements and a Ty4 transposon
 JOURNAL Yeast 12 (14), 1471-1474 (1996)
 MEDLINE [97103775](#)
 PUBMED [8948101](#)
 REMARK SEQUENCE FROM N.A.
 STRAIN=S288c / FY1679
 REFERENCE 3 (residues 1 to 337)
 AUTHORS Bun-Ya,M., Yompakdee,C., Shikata,K., Ogawa,N., Harashima,S. and
 Oshima,Y.
 TITLE Direct Submission
 JOURNAL Submitted (~AUG-1995)
 REMARK SEQUENCE OF 31-337 FROM N.A.
 STRAIN=GRF88
 COMMENT -----
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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] INVOLVED IN THE MITOCHONDRIAL EXPRESSION OF SUBUNITS 6
AND 8 OF THE FO-F1 ATP SYNTHASE.

[SUBCELLULAR LOCATION] Mitochondrial.

[SIMILARITY] BELONGS TO THE SUN FAMILY.

FEATURES Location/Qualifiers

 source 1..337
 /organism="Saccharomyces cerevisiae"
 /db_xref="taxon:4932"

 gene 1..337
 /gene="NCA3"
 /note="YJL116C; J0748"

 Protein 1..337
 /gene="NCA3"
 /product="NCA3 protein, mitochondrial precursor"

 Region (1.336)..337
 /gene="NCA3"
 /region_name="Mature chain"
 /note="NCA3 PROTEIN."

 Region 1..(2.337)
 /gene="NCA3"
 /region_name="Transit peptide"
 /note="MITOCHONDRION (POTENTIAL)."

 Region 61..64
 /gene="NCA3"
 /region_name="Domain"
 /note="POLY-THR."

ORIGIN

```
1 mkisaalils slssvafsap apapadshhe dhhkdekpav vtvtyidsn aatstvesaa
61 ttttlsssek dtseqkrdgg fqdgtvkcsd fpsvngivsl dwlgfggwas vmdmdantss
121 eckdgyycsy acepgmsktq wpsdqpsdgk svvglyckng ylyrtntdts dlcstdetsa
181 kainkksdsi alcrtdypgs enmviptvvd ggdsqpisvv dedtyyqwgg kktsaqqyyin
241 nagvsaedgc iwgtsgsdvg nwaplvlgag stngetylsl ipnpnsnqaa nfnvkivasd
301 ganvqgscay edgsftgdgs dgctvsvlsq saefvfy
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Oct 21 2002 11:56:56



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Boo

Search

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

Save

Text

Add to Clipboard

Get Subsequence

☐ 1: P25339. Hypothetical regu...[gi:1723801]

Links

LOCUS YGB4_YEAST 888 aa linear PLN 15-JUN-2002
 DEFINITION Hypothetical regulatory protein in PDR6-PDR1 intergenic region.
 ACCESSION P25339
 VERSION P25339 GI:1723801
 DBSOURCE swissprot: locus YGB4_YEAST, accession P25339;
 class: standard.
 created: May 1, 1992.
 sequence updated: Oct 1, 1996.
 annotation updated: Jun 15, 2002.
 xrefs: gi: 234326, gi: 234327, gi: 234321, gi: 4261598, gi:
 1322472, gi: 1322473, gi: 101509, gi: 422176
 xrefs (non-sequence databases): SGD S0002982, InterPro IPR001313,
 Pfam PF00806, SMART SM00025
 KEYWORDS Hypothetical protein; Transcription regulation; Zinc-finger;
 Metal-binding; Repeat.
 SOURCE baker's yeast.
 ORGANISM *Saccharomyces cerevisiae*
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (residues 1 to 888)
 AUTHORS Chen,W.N., Balzi,E., Capieaux,E. and Goffeau,A.
 TITLE The YGL023 gene encodes a putative regulatory protein
 JOURNAL Yeast 7 (3), 309-312 (1991)
 MEDLINE 91353086
 REMARK SEQUENCE FROM N.A.
 STRAIN=IL125-2B
 REFERENCE 2 (residues 1 to 888)
 AUTHORS Chen,W.N., Balzi,E., Capieaux,E., Choder,M. and Goffeau,A.
 TITLE The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1
 and ATE1 loci on chromosome VII from *Saccharomyces cerevisiae*
 reveals the PDR6 gene, a new member of the genetic network
 controlling pleiotropic drug resistance
 JOURNAL Yeast 7 (3), 287-299 (1991)
 MEDLINE 91353083
 REMARK SEQUENCE FROM N.A.
 STRAIN=IL125-2B
 REFERENCE 3 (residues 1 to 888)
 AUTHORS Hebling,U., Hofmann,B. and Delius,H.
 TITLE Direct Submission
 JOURNAL Submitted (~MAY-1996)
 REMARK SEQUENCE FROM N.A.
 COMMENT On Dec 11, 1996 this sequence version replaced gi:140711.

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 The original entry is available from <http://www.expasy.ch/sprot>

and <http://www.ebi.ac.uk/sprot>

[FUNCTION] Is not essential for haploid growth, but may affect diploid formation.

[SIMILARITY] BELONGS TO THE PUMILIO/MPT5 FAMILY.

[SIMILARITY] SOME, TO YEAST YJR091C.

FEATURES	Location/Qualifiers
<u>source</u>	1..888 /organism="Saccharomyces cerevisiae" /db_xref="taxon:4932"
<u>gene</u>	1..888 /gene="YGL014W" /note="YGL023"
<u>Protein</u>	1..888 /gene="YGL014W" /product="Hypothetical regulatory protein in PDR6-PDR1 intergenic region"
<u>Region</u>	8..38 /gene="YGL014W" /region_name="Domain" /note="ASP/GLU-RICH (ACIDIC)."
<u>Region</u>	471..542 /gene="YGL014W" /region_name="Domain" /note="ASN-RICH."
<u>Region</u>	521..535 /gene="YGL014W" /region_name="Domain" /note="POLY-ASN (POTENTIAL ACTIVATING DOMAIN)."
<u>Region</u>	571..583 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	595 /gene="YGL014W" /region_name="Conflict" /note="A -> R (IN REF. 1 AND 2)."
<u>Region</u>	607..619 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	643..655 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	679..691 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	716..728 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	724..742 /gene="YGL014W" /region_name="Zinc finger region" /note="C4-TYPE."
<u>Region</u>	752..764 /gene="YGL014W" /region_name="Repetitive region"
<u>Region</u>	831..843 /gene="YGL014W" /region_name="Repetitive region"

ORIGIN

1 mstkgkleei ddvpsvdpvv setvnsaleq lqlddpeena tsnafankvs qdsqfangpp

```
61 sqmfphpqmm ggmgfmpysq mmqvphnpcp ffpppdfndp taplssspln aggpplmfkn
121 dslpfqmlss gaavatqggq nlnplindns mkvlpiasad plwthsnvpg sasvaieett
181 atlqeslpsk gresnnkass frqrtfhals ptdlinaann vtlskdfqsd mqnfskakkp
241 svganntakt rtqsisfdnt psstsfippt nsvsekl sdf kietskedli nktapakkes
301 pttgyaaypy ggpllqpnp mpghphniss piygirspfp nsyemgaqfq pfspilnpts
361 hslnanspip ltqspihlap vlnpssnsva fsdmkndggk pttndkagp nvrmdlinpn
421 lgpsmqpfhi lppqqntppp pwlystpppf namvpphlla qnhmplmnsa nnkhhgrnnn
481 smsshndndn ignsnynnkd tgrsnvgkmm nmknsyhggy nnnnnnnnnn nnnnnsnatn
541 snsaeqrki eessrfadav ldqyigsihs lckdqhgcrf lqkqldilgs kaadaifeet
601 kdytvelmtd sfgnyliqkl leevtteqri vltkissphf veislphgt ralqklicci
661 ktdeeaqivv dslrpytvql skdlngnhvi qkclqrkpe nfqfifdais dscidiathr
721 hgccvlqrcl dhgtteqcdn lcdkllalvd kltldpfgny vvqyiitkea eknkydythk
781 ivhllkprai elsihkfgsn viekilktai vsepmlleil nnggetgiqs llndsygnyv
841 lqtaldishk qndylykrls eivapllvgp irntphgkri igmlhlhs
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Oct 21 2002 11:56:56